CRF Errors Corrected by the STIC Systems Branch

ENTERED

Serial Number: _10/026,706E_

CRF Processing Date: _4/9/2003_
Edited by: _AV_
Verified by: _AV_ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: _Inserted hard returns globally_
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 04/09/2003
PATENT APPLICATION: US/10/026,106E   TIME: 11:14:46

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\04092003\J026106E.raw**

```
   1 <110> APPLICANT: Renauld, Jean-Christophe
   2        Fickensicher, Helmut
   3        Dumoutier, Laure
   4        Hor, Simon
   6 <120> TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2
   8 <130> FILE REFERENCE: LUD 5752 NDH
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/026,106E
  12 <141> CURRENT FILING DATE: 2001-12-21
  14 <160> NUMBER OF SEQ ID NOS: 19
  16 <210> SEQ ID NO: 1
  17 <211> LENGTH: 21
  18 <212> TYPE: DNA
  19 <213> ORGANISM: Homo sapiens
W--> 20 <220> FEATURE:
W--> 21 <400> SEQUENCE: 1
  22 gggaaccaag gagctgctat g                          21
  24 <210> SEQ ID NO: 2
  25 <211> LENGTH: 21
  26 <212> TYPE: DNA
  27 <213> ORGANISM: Homo sapiens
W--> 28 <220> FEATURE:
W--> 29 <400> SEQUENCE: 2
  30 tggcactgag gcagtggtgt t                          21
  32 <210> SEQ ID NO: 3
  33 <211> LENGTH: 20
  34 <212> TYPE: DNA
  35 <213> ORGANISM: Homo sapiens
W--> 36 <220> FEATURE:
W--> 37 <400> SEQUENCE: 3
  38 aaggccatgg cggggcccga                            20
  40 <210> SEQ ID NO: 4
  41 <211> LENGTH: 20
  42 <212> TYPE: DNA
  43 <213> ORGANISM: Homo sapiens
W--> 44 <220> FEATURE:
W--> 45 <400> SEQUENCE: 4
  46 cagaaggtca gtgtctgaag                            20
  48 <210> SEQ ID NO: 5
  49 <211> LENGTH: 21
  50 <212> TYPE: DNA
  51 <213> ORGANISM: Homo sapiens
W--> 52 <220> FEATURE:
W--> 53 <400> SEQUENCE: 5
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```
RAW SEQUENCE LISTING          DATE: 04/09/2003
PATENT APPLICATION:  US/10/026,106E    TIME: 11:14:46

    Input Set : A:\PTO.AMC.txt
    Output Set: N:\CRF4\04092003\J026106E.raw
```

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        56 <210> SEQ ID NO: 6
        57 <211> LENGTH: 21
        58 <212> TYPE: DNA
        59 <213> ORGANISM: Homo sapiens
W--> 60 <220> FEATURE:
W--> 61 <400> SEQUENCE: 6
        62 catcagattc ggtgggatgt c                                21
        64 <210> SEQ ID NO: 7
        65 <211> LENGTH: 1599
        66 <212> TYPE: DNA
        67 <213> ORGANISM: Homo sapiens
W--> 68 <220> FEATURE:
W--> 69 <400> SEQUENCE: 7
        71 aaggccatgg cggggcccga gcgctggggc cccctgctcc tgtgcctgct gcaggccgct 60
        72 ccagggaggc cccgtctggc ccctccccag aatgtgacgc tgctctccca gaacttcagc 120
        73 gtgtacctga catggctcc caggggcttggc aaccccagg atgtgaccta ttttgtggcc 180
        74 atcagagctc tcccacccgt agacggtggc gcgaagtgga agagtgtgcg ggaaccaagg 240
        75 agctgctatg ttctatgatg tgcctgaaga aacaggacct gtacaacaag ttcaagggac 300
        76 gcgtgcggac ggtttctccc agctccaagt cccccctgggt ggagtccgaa tacctggatt 360
        77 acctttttga agtggagccg gcccccacctg tcctggtgct cacccagacg gaggagatcc 420
        78 tgagtgccaa tgccacgtac cagctgcccc cctgcatgcc cccactggat ctgaagtatg 480
        79 aggtggcatt ctggaaggag ggggccggaa acaagaccct atttccagtc actccccatg 540
        80 gccagccagt ccagatcact ctccagccag ctgccagcga acaccactgc ctcagtgcca 600
        81 gaaccatcta cacgttcagt gtcccgaaat acagcaagtt ctctaagccc acctgcttct 660
        82 tgctggaggt cccagaagcg aactgggctt tcctggtgct gccatcgctt ctgatactgc 720
        83 tgttagtaat tgccgcaggg ggtgtgatct ggaagaccct catggggaac ccctggtttc 780
        84 agcgggcaaa gatgccacgg gccctggact tttctggaca cacacaccct gtggcaacct 840
        85 ttcagcccag cagaccagag tccgtgaatg acttgttcct ctgtccccaa aaggaactga 900
        86 ccagaggggt caggccgacg cctcgagtca gggccccagc cacccaacag acaagatgga 960
        87 agaaggacct tgcagaggac gaagaggagg aggatgagga ggacacagaa gatggcgtca 1020
        88 gcttccagcc ctacattgaa ccaccttctt tcctggggca agagcaccag gctccagggc 1080
        89 actcggaggc tggtgggggtg gactcaggga ggcccagggc tcctctggtc ccaagcgaag 1140
        90 gctcctctgc ttgggattct tcagacagaa gctgggccag cactgtggac tcctcctgggg 1200
        91 acagggctgg gtcctctggc tatttggctg agaaggggcc aggccaaggg ccgggtgggg 1260
        92 atgggcacca agaatctctc ccaccacctg aattctccaa ggactcgggt ttcctggaag 1320
        93 agctcccaga agataacctc tcctcctggg ccacctgggg caccttacca ccggagccga 1380
        94 atctggtccc tgggggaccc ccagtttctc ttcagacact gaccttctgc tgggaaagca 1440
        95 gccctgagga ggaagaggag gcgagggaat cagaaattga ggacagcgat gcgggcagct 1500
        96 ggggggctga gagcacccag aggaccgagg acaggggccg gacattgggg cattacatgg 1560
        97 ccaggtgagc tgtcccccga catcccaccg aatctgatg        1599
       101 <210> SEQ ID NO: 8
       102 <211> LENGTH: 522
       103 <212> TYPE: PRT
       104 <213> ORGANISM: Homo sapiens
W--> 105 <220> FEATURE:
W--> 106 <400> SEQUENCE: 8
       107 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
       108 1               5                   10                  15
```

RAW SEQUENCE LISTING   DATE: 04/09/2003
PATENT APPLICATION: US/10/026,106E   TIME: 11:14:46

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\04092003\J026106E.raw

```
109 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
110              20              25              30
111 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
112          35              40              45
113 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
114      50              55              60
115 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
116 65              70              75              80
117 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
118              85              90              95
119 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
120          100             105             110
121 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
122          115             120             125
123 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
124      130             135             140
125 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
126 145             150             155             160
127 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
128              165             170             175
129 Pro His Val Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro
130              180             185             190
131 Ala Ala Ser Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe
132          195             200             205
133 Ser Val Pro  Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu
134      210             215             220
135 Glu Val Pro Glu Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu
136 225             230             235             240
137 Ile Leu Leu Leu Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu
138              245             250             255
139 Met Gly Asn Pro Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp
140              260             265             270
141 Phe Ser Gly His Thr Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg
142          275             280             285
143 Pro Glu Ser Val Asn Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr
144      290             295             300
145 Arg Gly Val Arg Pro Thr Pro Arg Val Arg Pro Ala Thr Gln Gln Thr
146 305             310             315             320
147 Arg Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Asp Thr Glu
148              325             330             335
149 Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly
150              340             345             350
151 Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser
152          355             360             365
153 Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp
154      370             375             380
155 Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp
156 385             390             395             400
157 Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly
```

```
158                    405                  410                  415
159 Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser
160                    420                  425                  430
161 Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser
162            435                  440                  445
163 Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Pro Asn Leu Val Pro
164     450                  455                  460
165 Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser
166 465                  470                  475                  480
167 Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser
168                    485                  490                  495
169 Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg
170            500                  505                  510
171 Gly Arg Thr Leu Gly His Tyr Met Ala Arg
172        515                  520
174 <210> SEQ ID NO: 9
175 <211> LENGTH: 1469
176 <212> TYPE: DNA
177 <213> ORGANISM: Homo sapiens
```
W--> 178 **<220> FEATURE:**
W--> 179 **<400> SEQUENCE: 9**
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182 aaggccatgg cggggcccga gcgctggggc cccctgctcc tgtgcctgct gcaggccgct  60
183 ccagggaggc cccgtctggc ccctccccag aatgtgacgc tgctctccca gaacttcagc 120
184 gtgtacctga catggctccc agggcttggc aacccccagg atgtgaccta ttttgtggcc 180
185 tatcagagct ctcccacccg tagacggtgg cgcgaagtgg aagagtgtgc gggaaccaag 240
186 gagctgctat gttctatgat gtgcctgaag aaacaggacc tgtacaacaa gttcaaggga 300
187 cgcgtgcgga cggtttctcc cagctccaag tccccctggg tggagtccga atacctggat 360
188 tacctttttg aagtggagcc ggccccacct gtcctggtgc tcacccagac ggaggagatc 420
189 ctgagtgcca atgccacgta ccagctgccc ccctgcatgc ccccactgga tctgaagtat 480
190 gaggtggcat tctggaagga gggggccgga aacaagaccc tatttccagt cactccccat 540
191 ggccagccag tccagatcac tctccagcca gctgccagcg aacaccactg cctcagtgcc 600
192 agaaccatct acacgttcag tgtcccgaaa tacagcaagt tctctaagcc cacctgcttc 660
193 ttgctggagg tcccaggact tttctggaca cacacaccct gtggcaacct ttcagcccag 720
194 cagaccagag tccgtgaatg acttgttcct ctgtccccaa aaggaactga ccagagtggt 780
195 caggccgacg cctcgagtca gggccccagc cacccaacag acaagatgga agaaggacct 840
196 tgcagaggac gaagaggagg aggatgagga ggacacagaa gatggcgtca gcttccagcc 900
197 ctacattgaa ccaccttctt tcctggggca agagcaccag gctccagggc actcggaggc 960
199 tggtggggtg gactcaggga ggcccagggc tcctctggtc ccaagcgaag gctcctctgc1020
200 ttgggattct tcagacagaa gctgggccag cactgtggac tcctcctggg acagggctgg1080
201 gtcctctggc tatttggctg agaaggggcc aggccaaggg ccgggtgggg atgggcacca1140
202 agaatctctc ccaccacctg aattctccaa ggactcgggt ttcctggaag agctcccaga1200
203 agataacctc tcctcctggg ccacctgggg caccttacca ccggagccga atctggtccc1260
204 tgggggaccc ccagtttctc ttcagacact gaccttctgc tgggaaagca gccctgagga1320
205 ggaagaggag gcgagggaat cagaaattga ggacagcgat gcgggcagct gggggggctga1380
206 gagcacccag aggaccgagg acaggggccg gacattgggg cattacatgg ccaggtgagc1440
207 tgtcccccga catcccaccg aatctgatg            1469
212 <210> SEQ ID NO: 10
213 <211> LENGTH: 244
214 <212> TYPE: PRT
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      215 <213> ORGANISM: Homo sapiens
W-->  216 <220> FEATURE:
W-->  217 <400> SEQUENCE: 10
      219 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
      220 1               5                   10                  15
      221 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
      222             20                  25                  30
      223 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
      224         35                  40                  45
      225 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
      226     50                  55                  60
      227 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
      228 65                  70                  75                  80
      229 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
      230             85                  90                  95
      231 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
      232             100                 105                 110
      233 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
      234         115                 120                 125
      235 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
      236     130                 135                 140
      237 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
      238 145                 150                 155                 160
      239 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
      240             165                 170                 175
      241 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
      242             180                 185                 190
      243 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
      244         195                 200                 205
      245 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Gly
      246     210                 215                 220
      247 Leu Phe Trp Thr His Thr Pro Cys Gly Asn Leu Ser Ala Gln Gln Thr
      248 225                 230                 235                 240
      249 Arg Val Arg Glu
      251 <210> SEQ ID NO: 11
      252 <211> LENGTH: 21
      253 <212> TYPE: DNA
      254 <213> ORGANISM: Homo sapiens
W-->  255 <220> FEATURE:
W-->  256 <400> SEQUENCE: 11
      257 ttcagtgtcc cgaaatacag c                              21
      259 <210> SEQ ID NO: 12
      260 <211> LENGTH: 20
      261 <212> TYPE: DNA
      262 <213> ORGANISM: Homo sapiens
W-->  263 <220> FEATURE:
W-->  264 <400> SEQUENCE: 12
      265 aagaaggtgg ttcaatgtag                                20
      267 <210> SEQ ID NO: 13
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VERIFICATION SUMMARY   DATE: 04/09/2003
PATENT APPLICATION: **US/10/026,106E**   TIME: 11:14:47

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\04092003\J026106E.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Current Application Number
L:20  M:283 W: Missing Blank Line separator, <220> field identifier
L:21  M:283 W: Missing Blank Line separator, <400> field identifier
L:28  M:283 W: Missing Blank Line separator, <220> field identifier
L:29  M:283 W: Missing Blank Line separator, <400> field identifier
L:36  M:283 W: Missing Blank Line separator, <220> field identifier
L:37  M:283 W: Missing Blank Line separator, <400> field identifier
L:44  M:283 W: Missing Blank Line separator, <220> field identifier
L:45  M:283 W: Missing Blank Line separator, <400> field identifier
L:52  M:283 W: Missing Blank Line separator, <220> field identifier
L:53  M:283 W: Missing Blank Line separator, <400> field identifier
L:60  M:283 W: Missing Blank Line separator, <220> field identifier
L:61  M:283 W: Missing Blank Line separator, <400> field identifier
L:68  M:283 W: Missing Blank Line separator, <220> field identifier
L:69  M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:178 M:283 W: Missing Blank Line separator, <220> field identifier
L:179 M:283 W: Missing Blank Line separator, <400> field identifier
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:217 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:283 W: Missing Blank Line separator, <220> field identifier
L:256 M:283 W: Missing Blank Line separator, <400> field identifier
L:263 M:283 W: Missing Blank Line separator, <220> field identifier
L:264 M:283 W: Missing Blank Line separator, <400> field identifier
L:271 M:283 W: Missing Blank Line separator, <220> field identifier
L:272 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:283 W: Missing Blank Line separator, <220> field identifier
L:280 M:283 W: Missing Blank Line separator, <400> field identifier
L:288 M:283 W: Missing Blank Line separator, <220> field identifier
L:289 M:283 W: Missing Blank Line separator, <400> field identifier
L:296 M:283 W: Missing Blank Line separator, <220> field identifier
L:297 M:283 W: Missing Blank Line separator, <400> field identifier
L:304 M:283 W: Missing Blank Line separator, <220> field identifier
L:305 M:283 W: Missing Blank Line separator, <400> field identifier
L:312 M:283 W: Missing Blank Line separator, <220> field identifier
L:313 M:283 W: Missing Blank Line separator, <400> field identifier
L:320 M:283 W: Missing Blank Line separator, <220> field identifier
L:321 M:283 W: Missing Blank Line separator, <400> field identifier
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OIPE

RAW SEQUENCE LISTING   DATE: 04/07/2003
PATENT APPLICATION: US/10/026,106E   TIME: 07:15:45

Input Set : **A:\LUD 5752. Ascii Seq**
Output Set: **N:\CRF4\04042003\J026106E.raw**

```
  1 <110> APPLICANT: Renauld, Jean-Christophe
  2        Fickensicher, Helmut
  3        Dumoutier, Laure
  4        Hor, Simon
  6 <120> TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2
  8 <130> FILE REFERENCE: LUD 5752 NDH
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/026,106E
 12 <141> CURRENT FILING DATE: 2001-12-21
 14 <160> NUMBER OF SEQ ID NOS: 19
```

ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed

```
     101 <210> SEQ ID NO: 8
     102 <211> LENGTH: 522
     103 <212> TYPE: PRT
     104 <213> ORGANISM: Homo sapiens
W--> 105 <220> FEATURE:
W--> 106 <400> SEQUENCE: 8
     107 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
     108 1               5                   10           .          15
     109 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
     110             20                  25                  30
     111 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
     112         35              40                  45
     113 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
     114         50              55                  60
     115 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
E--> 116
65                  70                  75              80    Leu Cys Ser Met Met Cys Leu
E--> 117             85              90                  95
     118 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 119             100             105                 110
     120 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 121         115             120                 125
     122 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 123     130             135                 140
     124 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 125
145                 150             155             160    Ala Phe Trp Lys Glu Gly Ala Gly Asn
E--> 126             165             170                 175
     127 Pro His Val Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro
E--> 128             180             185                 190
     129 Ala Ala Ser Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe
```

insert hard return (handwritten annotation)

E--> 130   195   200   205

RAW SEQUENCE LISTING   DATE: 04/07/2003
PATENT APPLICATION: US/10/026,106E TIME: 07:15:45

Input Set : A:\LUD 5752. Ascii Seq
Output Set: N:\CRF4\04042003\J026106E.raw

```
        131 Ser Val Pro  Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu
E--> 132     210             215             220         .
        133 Glu Val Pro Glu Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu
E--> 134 225             230             235             240
        135 Ile Leu Leu Leu Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu
E--> 136             .   245             250             255
        137 Met Gly Asn Pro Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp
E--> 138             260             265             270
        139 Phe Ser Gly His Thr Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg
E--> 140         275             280             285
        141 Pro Glu Ser Val Asn Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr
E--> 142     290             295             300
        143 Arg Gly Val Arg Pro Thr Pro Arg Val Arg Pro Ala Thr Gln Gln Thr
E--> 144 305             310             315             320
        145 Arg Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Thr Glu
E--> 146             325         .       330             335
        147 Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly
E--> 148             340             345             350
        149 Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser
E--> 150         355             360             365
        151 Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp
E--> 152     370             375             380         .
        153 Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp
E--> 154 385             390     .           395             400
        155 Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly
E--> 156             405             410             415
        157 Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser
E--> 158     .       420             425             430
        159 Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser
E--> 160         435             440             445
        161 Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Pro Asn Leu Val Pro
E--> 162     450             455             460
        163 Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser
E--> 164 465             470             475             480
        165 Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser
E--> 166             485             490             495
        167 Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg
E--> 168         500             505             510
        169 Gly Arg Thr Leu Gly His Tyr Met Ala Arg
E--> 170         515             520
        172 <210> SEQ ID NO: 9
        173 <211> LENGTH: 1469
        174 <212> TYPE: DNA
        175 <213> ORGANISM: Homo sapiens
W--> 176 <220> FEATURE:
W--> 177 <400> SEQUENCE: 9
        180 aaggccatgg cggggcccga gcgctggggc cccctgctcc tgtgcctgct gcaggccgct 60
        181 ccagggaggc cccgtctggc ccctccccag aatgtgacgc tgctctccca gaacttcagc 120
        182 gtgtacctga catggctccc agggcttggc aacccccagg atgtgaccta ttttgtggcc 180
```

```
183 tatcagagct ctcccacccg tagacggtgg cgcgaagtgg aagagtgtgc gggaaccaag 240
184 gagctgctat gttctatgat gtgcctgaag aaacaggacc tgtacaacaa gttcaaggga 300
185 cgcgtgcgga cggtttctcc cagctccaag tcccctgggg tggagtccga atacctggat 360
186 tacctttttg aagtggagcc ggccccacct gtcctggtgc tcacccagac ggaggagatc 420
187 ctgagtgcca atgccacgta ccagctgccc ccctgcatgc ccccactgga tctgaagtat 480
188 gaggtggcat tctggaagga ggggggccgga aacaagaccc tatttccagt cactccccat 540
189 ggccagccag tccagatcac tctccagcca gctgccagcg aacaccactg cctcagtgcc 600
190 agaaccatct acacgttcag tgtcccgaaa tacagcaagt tctctaagcc cacctgcttc 660
191 ttgctggagg tcccaggact tttctggaca cacacaccct gtggcaacct ttcagcccag 720
192 cagaccagag tccgtgaatg acttgttcct ctgtccccaa aaggaactga ccagaggggt 780
193 caggccgacg cctcgagtca gggccccagc cacccaacag acaagatgga agaaggacct 840
194 tgcagaggac gaagaggagg aggatgagga ggacacagaa gatggcgtca gcttccagcc 900
```

E--> 195

ctacattgaa ccaccttctt tcctggggca agagcaccag gctccagggc actcggaggc 960 ⤳tggtggggtg gactcaggga gⓒ

```
196 ttgggattct tcagacagaa gctgggccag cactgtggac tcctcctggg acagggctgg1080
197 gtcctctggc tatttggctg agaaggggcc aggccaaggg ccgggtgggg atgggcacca1140
198 agaatctctc ccaccacctg aattctccaa ggactcgggt ttcctggaag agctcccaga1200
199 agataacctc tcctcctggg ccacctgggg caccttacca ccggagccga atctggtccc1260
200 tggggaccc ccagtttctc ttcagacact gaccttctgc tgggaaagca gccctgagga1320
201 ggaagaggag gcgagggaat cagaaattga ggacagcgat gcgggcagct ggggggctga1380
202 gagcacccag aggaccgagg acaggggccg gacattgggg cattacatgg ccaggtgagc1440
203 tgtcccccga catcccaccg aatctgatg          1469
208 <210> SEQ ID NO: 10
209 <211> LENGTH: 244
210 <212> TYPE: PRT
211 <213> ORGANISM: Homo sapiens
```

W--> 212 <220> FEATURE:
W--> 213 <400> SEQUENCE: 10

```
215 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
216 1               5               10              15
217 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
218             20              25              30
219 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
220         35              40              45
221 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
222     50              55              60
223 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
```

E--> 224
65   70   75   80 ⤳ Leu Cys Ser Met Met Cys Leu
E--> 225   85   90   95

```
226 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
```

E--> 227   100   105   110

```
228 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
```

E--> 229   115   120   125

```
230 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
```

E--> 231   130   135   140

```
232 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
```

E--> 233 145   150   155   160

```
234 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
```

E--> 235   165   170   175

```
236 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
```

RAW SEQUENCE LISTING   DATE: 04/07/2003
PATENT APPLICATION: US/10/026,106E   TIME: 07:15:45

Input Set : **A:\LUD 5752. Ascii Seq**
Output Set: **N:\CRF4\04042003\J026106E.raw**

```
E--> 237              180                 185                 190
     238 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
E--> 239              195                 200                 205
     240 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Gly
E--> 241      210                 215                 220
     242 Leu Phe Trp Thr His Thr Pro Cys Gly Asn Leu Ser Ala Gln Gln Thr
E--> 243 225                 230                 235                 240
     244 Arg Val Arg Glu
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/07/2003
PATENT APPLICATION: **US/10/026,106E**   TIME: 07:15:46

Input Set : **A:\LUD 5752. Ascii Seq**
Output Set: **N:\CRF4\04042003\J026106E.raw**

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:8; Line(s) 116,125
Seq#:9; Line(s) 195
Seq#:10; Line(s) 224

VERIFICATION SUMMARY   DATE: 04/07/2003
PATENT APPLICATION: **US/10/026,106E**   TIME: 07:15:46

Input Set : **A:\LUD 5752. Ascii Seq**
Output Set: **N:\CRF4\04042003\J026106E.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:283 W: Missing Blank Line separator, <400> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:53 M:283 W: Missing Blank Line separator, <400> field identifier
L:60 M:283 W: Missing Blank Line separator, <220> field identifier
L:61 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:283 W: Missing Blank Line separator, <220> field identifier
L:69 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:116 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:116 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=8
L:176 M:283 W: Missing Blank Line separator, <220> field identifier
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:195 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:212 M:283 W: Missing Blank Line separator, <220> field identifier
L:213 M:283 W: Missing Blank Line separator, <400> field identifier
L:224 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:224 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=10
L:250 M:283 W: Missing Blank Line separator, <220> field identifier
L:251 M:283 W: Missing Blank Line separator, <400> field identifier
L:258 M:283 W: Missing Blank Line separator, <220> field identifier
L:259 M:283 W: Missing Blank Line separator, <400> field identifier
L:266 M:283 W: Missing Blank Line separator, <220> field identifier
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:274 M:283 W: Missing Blank Line separator, <220> field identifier
L:275 M:283 W: Missing Blank Line separator, <400> field identifier
L:283 M:283 W: Missing Blank Line separator, <220> field identifier
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:283 W: Missing Blank Line separator, <220> field identifier
L:292 M:283 W: Missing Blank Line separator, <400> field identifier
L:299 M:283 W: Missing Blank Line separator, <220> field identifier
L:300 M:283 W: Missing Blank Line separator, <400> field identifier
L:307 M:283 W: Missing Blank Line separator, <220> field identifier
L:308 M:283 W: Missing Blank Line separator, <400> field identifier
L:315 M:283 W: Missing Blank Line separator, <220> field identifier
L:316 M:283 W: Missing Blank Line separator, <400> field identifier
```